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      Krause, James
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Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr 305 310 315 320

Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Asn 325 330 335

Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met 340 345 350

Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser 355 360 365

Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn Glu Lys Ile 370 375 380

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His Leu Pro Leu Ala Val Ile Phe Thr Leu Ala Leu Ala Tyr Gly Ala 35 40 45

Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile 50 55 60

Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val Asn 65 70 75 80

Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys Leu Pro Phe Thr 85 90 95

Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Thr Met Cys 100 105 110

Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile Phe 115 120 125

Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn Pro 130 135 140

Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile Gly Ile Thr Val 145 150 155 160

Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Val Ile Tyr Gln

165 170 175

Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu Ala Ala Phe Lys 180 185 190

Asp Lys Tyr Val Cys Phe Asp Lys Phe Pro Ser Asp Ser His Arg Leu
195 200 205

Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys 210 215 220

Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg Arg 225 230 235 240

Asn Asn Met Met Asp Lys Ile Arg Asp Ser Lys Tyr Arg Ser Ser Glu 245 250 255

Thr Lys Arg Ile Asn Val Met Leu Leu Ser Ile Val Val Ala Phe Ala 260 265 270

Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp Asn 275 280 285

His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu Cys 290 295 300

His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr Gly 305 310 315 320

Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Asn Phe 325 330 335

Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser 340 345 350

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tgggctctat acatttgtaa gtcttcttgg ctttatgggg aatctactta ttttaatggc 240
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Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp 35 40 45

Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu 50 55 60

Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg
65 70 75 80

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser 85 90 95

Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val $100 \ \ 105 \ \ 110$

Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro 115 120 125

Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser 130 135 140

Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu
165 170 175

Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu 180 185 190

Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys 195 200 205

Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser 210 215 220

Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser 235 230 235

His Thr Ser Val Cys Ile Arg Leu Lys Arg Arg Asn Asn Met Met Asp $245 \\ 250 \\ 255$

Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser Arg Ser Arg Ser Val Phe 260 265 270

Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro 275 280 285

Leu His Leu Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile Ser 290 295 300

Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly Met 305 310 315 320

- Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu 165 170 175
- Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu 180 185 190
- Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys 195 200 205
- Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser 210 215 220
- Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser 225 230 235 240
- His Thr Ser Val Cys Arg Ser Ile Ser Cys Gly Leu Ser Asn Lys Glu 245 250 255
- Asn Arg Leu Glu Glu Asn Glu Met Ile Asn Leu Thr Leu His Pro Ser 260 265 270
- Lys Lys Ser Gly Pro Gln Val Lys Leu Ser Gly Ser His Lys Trp Ser 275 280 285
- Tyr Ser Phe Ile Lys Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala 290 295 300
- Cys Val Leu Pro Ala Pro Glu Arg Pro Ser Gln Glu Asn His Ser Arg 305 310 315 320
- Ile Leu Pro Glu Asn Phe Gly Ser Val Arg Ser Gln Leu Ser Ser Ser 325 330 335
- Ser Lys Phe Ile Pro Gly Val Pro Thr Cys Phe Glu Ile Lys Pro Glu 340 345 350
- Glu Asn Ser Asp Val His Glu Leu Arg Val Lys Arg Ser Val Thr Arg 355 360 365
- Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile 370 375 380
- Leu Val Phe Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val 385 390 395 400
- Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val 405 410 415
- Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro 420 425 430
- Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Gln Arg Asp Leu Gln Phe 435 440 445
- Phe Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr 450 455 460

Ile Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys 465 470 475 480

Gln Ala Ser Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn 485 490 495

Glu Lys Ile

<210> 10

<211> 394

<212> PRT

<213> Artificial Sequence

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Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp 35 40 45

Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu 50 60

Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg 65 70 75 80

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser 85 90 95

Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val $100 \,$ $105 \,$ $110 \,$

Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro 115 120 125

Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser 130 135 140

Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu 165 170 175

Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu \$180\$

Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys

195 200 205

Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser 210 215 220

Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser 225 230 235 240

Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser Arg Ser Arg Ser Val Phe 260 265 270

Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro 275 280 285

Leu His Leu Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile Ser 290 295 300

Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly Met 305 310 315 320

Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn Gly 325 330 335

Ile Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe Cys Asp Phe Arg Ser 340 345 350

Arg Asp Asp Tyr Glu Thr Ile Ala Met Ser Thr Met His Thr Asp 355 360 365

Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala Phe Lys Lys 370 375 380

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<213> Artificial Sequence

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<400> 11

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<211> 8

<212> PRT

<213> Artificial Sequence

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<210> 13 <211> 455 <212> PRT

<213> Homo sapiens

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Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp

Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu

Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser

Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val 100

Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro 120

Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser 135

Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn 155 150

Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu 170 165

Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu 185

Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys 200 195

Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser 215

Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser 225 230 235 His Thr Ser Val Cys Arg Ser Ile Ser Cys Gly Leu Ser Asn Lys Glu 250 Asn Arg Leu Glu Glu Asn Glu Met Ile Asn Leu Thr Leu His Pro Ser 260 265 Lys Lys Ser Gly Pro Gln Val Lys Leu Ser Gly Ser His Lys Trp Ser Tyr Ser Phe Ile Lys Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala Pro Glu Arg Pro Ser Gln Glu Asn His Ser Arg 310 Ile Leu Pro Glu Asn Phe Gly Ser Val Arg Ser Gln Leu Ser Ser Ser 330 Ser Lys Phe Ile Pro Gly Val Pro Thr Cys Phe Glu Ile Lys Pro Glu Glu Asn Ser Asp Val His Glu Leu Arg Val Lys Arg Ser Val Thr Arg Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val 410 Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro 425 Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Lys Ala Asp Leu Val Ser 435 440 Leu Ile His Cys Leu His Met

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Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr 35 40 45

Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met 50 55 60

Ala Leu Met Arg Lys Arg Asn Gln Lys Thr Met Val Asn Phe Leu Ile 65 70 75 80

Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val 100 105 110

Met Cys His Ile Met Pro Phe Leu Gl
n Cys Val Ser Val Leu Val Ser 115 120 125

Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys 130 135 140

His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile 145 150 155 160

Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val 165 170 175

Phe His Ser Leu Val Glu Leu Gln Glu Thr Phe Asp Ser Ala Leu Leu 180 185 190

Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg 195 200 205

Ile Ala Phe Thr Ile Ser Leu Leu Val Gln Tyr Ile Leu Pro Leu 210 215 220

Val Cys Leu Thr Val Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg

225 230 235 240

Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser 245 250 255

Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe 260 265 270

Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val Thr Asp Phe 275 280 285

Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile 290 295 300

Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr 305 310 315 320

Gly Phe Leu Asn Asn Gly Ile Lys Ala Asp Leu Ile Ser Leu Ile Gln 325 330 335

Cys Leu His Met Ser 340

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<213> Artificial Sequence

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Asn Asn Thr Ala Ala Thr Arg Asn Ser Asp Phe Pro Val Trp Asp Asp 20 25 30

Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr 35 40 45

Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met 50 60

Ala Leu Met Arg Lys Arg Asn Gln Lys Thr Met Val Asn Phe Leu Ile
65 70 75 80

Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro 85 90 95

Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val
100 105 110

Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser 115 120 125

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gatgactata aaagcagtgt agatgactta cagtattttc tgattgggct ctatacattt 180
qtaaqtette ttqqctttat qqqqaateta ettattttaa tqqeteteat qaaaaaqeqt 240
aatcagaaga ctacggtaaa cttcctcata ggcaatctgg ccttttctga tatcttggtt 300
gtgctgtttt gctcaccttt cacactgacg tctgtcttgc tggatcagtg gatgtttggc 360
aaagtcatgt gccatattat gccttttctt caatgtgtgt cagttttggt ttcaacttta 420
attitaatat caattgccat tgtcaggtat catatgataa aacatcccat atctaataat 480
ttaacagcaa accatggeta etttetgata getaetgtet ggacaetagg ttttgeeate 540
tgttctcccc ttccagtgtt tcacagtctt gtggaacttc aagaaacatt tggttcagca 600
ttgctgagca gcaggtattt atgtgttgag tcatggccat ctgattcata cagaattgcc 660
tttactatct ctttattgct agttcagtat attctgccct tagtttgtct tactgtaagt 720
catacaagtg totgcagaag tataagotgt ggattgtoca acaaagaaaa cagacttgaa 780
gaaaatgaga tgatcaactt aactcttcat ccatccaaaa agagtgggcc tcaggtgaaa 840
ctctctggca gccataaatg gagttattca ttcatcaaaa aacacagaag aagatatagc 900
aagaagacag catgtgtgtt acctgctcca gaaagacctt ctcaagagaa ccactccaga 960
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ccaggggtcc ccacttgctt tgagataaaa cctgaagaaa attcagatgt tcatgaattg 1080
agagtaaaac gttctgttac aagaataaaa aagagatctc gaagtgtttt ctacagactg 1140
accatactga tattagtatt tgctgttagt tggatgccac tacacctttt ccatgtggta 1200
actgatttta atgacaatct tatttcaaat aggcatttca agttggtgta ttgcatttgt 1260
catttgttgg gcatgatgtc ctgttgtctt aatccaattc tatatgggtt tcttaataat 1320
ggaattcaga gagacttgca gttcttcttc aacttttgtg atttccggtc tcgggatgat 1380
gattatgaaa caatagccat gtccacgatg cacacagatg tttccaaaaac ttctttgaag 1440
caagcaagcc cagtcqcatt taaaaaaaatc aacaacaatg atgataatga aaaaatctga 1500
<210> 8
<211> 1201
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Y5/Y1 CHIMERA
<400> 8
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cgacgagtat tataacaaga cacttgccac agagaataat actgctgcca ctcggaattc 120
tgatttccca gtctgggatg actataaaag cagtgtagat gacttacagt attttctgat 180
tgggctctat acatttgtaa gtcttcttgg ctttatgggg aatctactta ttttaatggc 240
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Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys
130 135 140

His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile 145 150 150

Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val 165 170 175

Phe His Ser Leu Val Glu Leu Gln Glu Thr Phe Asp Ser Ala Leu Leu 180 185 190

Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg 195 200 205

Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu 210 215 220

Val Cys Leu Thr Val Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg 225 230 235 240

Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser 245 250 255

Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe 260 265 270

Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val Thr Asp Phe 275 280 285

Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile 290 295 300

Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr 305 310 315 320

Gly Phe Leu Asn Asn Gly Ile Gln Arg Asp Leu Gln Phe Phe Asn \$325\$ \$330 \$35

Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met 340 345 350

Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser 355 360 365

Pro Val Ala Phe Lys Lys Ile Asn Asn Asp Asp Asn Glu Lys Ile 370 375 380

<210> 22

<211> 508

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 22
Met Glu Val Lys Leu Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu
10 15

Asn Asn Thr Ala Ala Ser Gln Asn Thr Ala Ser Pro Ala Trp Glu Asp
20 25 30

Tyr Arg Gly Thr Glu Asn Asn Thr Ser Ala Ala Arg Asn Thr Ala Phe 35 40 45

Pro Val Trp Glu Asp Tyr Arg Gly Ser Val Asp Asp Leu Gln Tyr Phe 50 55 60

Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn 65 70 75 80

Leu Leu Ile Leu Met Ala Val Met Lys Lys Arg Asn Gln Lys Thr Thr 85 90 95

Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val 100 105 110

Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp 115 120 125

Met Phe Gly Lys Ala Met Cys His Ile Met Pro Phe Leu Gln Cys Val 130 135 140

Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg 145 150 155 160

Tyr His Met Ile Lys His Pro Ile Ser Asn Asn Leu Thr Ala Asn His 165 170 175

Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys $180 \hspace{1cm} 185 \hspace{1cm} 190$

Ser Pro Phe Pro Val Phe His Ser Leu Val Glu Leu Lys Glu Thr Phe 195 200 205

Gly Ser Ala Leu Leu Ser Ser Lys Tyr Leu Cys Val Glu Ser Trp Pro 210 215 220

Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln 225 230 235 240

Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser His Thr Ser Val Cys \$245\$ \$250\$

Arg Ser Ile Ser Cys Gly Leu Ser His Lys Glu Asn Arg Leu Glu Glu 260 265 270

Asn Glu Met Ile Asn Leu Thr Leu His Pro Ser Lys Lys Ser Arg Asp 275 280 285

Gln Ala Lys Pro Pro Ser Thr Gln Lys Trp Ser Tyr Ser Phe Ile Arg 290 295 300

Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala 305 310 315 320

Gly Ser Val Arg Ser Gln Leu Ser Pro Ser Ser Lys Val Ile Pro Gly 340 345 350

Val Pro Ile Cys Phe Glu Val Lys Pro Glu Glu Ser Ser Asp Ala Gln 355 360 365

Glu Met Arg Val Lys Arg Ser Leu Thr Arg Ile Lys Lys Arg Ser Arg 370 375 380

Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser 385 390 395 400

Trp Met Pro Leu His Val Phe His Val Val Thr Asp Phe Asn Asp Asn $405 \hspace{1.5cm} 410 \hspace{1.5cm} 415$

Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu 420 425 430

Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu 435 440 445

Asn Asn Gly Ile Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe Cys Asp 450 455 460

Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser Thr Met 465 470 475 480

His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala 485 490 495

Phe Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Val 500 505

<210> 23

<211> 352

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Y1/Y5 CHIMERA

<400> 23

Met Asp Val Leu Phe Phe His Gln Asp Ser Ser Met Glu Phe Lys Leu 1 5 10 15

Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu Asn Asn Thr Ala Ala 20 25 30

Ala Arg Asn Ala Ala Phe Pro Ala Trp Glu Asp Tyr Arg Gly Ser Val

35	40	45

Asp	Asp 50	Leu	Gln	Tyr	Phe	Leu 55	Ile	Gly	Leu	Tyr	Thr 60	Phe	Val	Ser	Leu
Leu 65	Gly	Phe	Met	Gly	Asn 70	Leu	Leu	Ile	Leu	Met 75	Ala	Val	Met	Lys	Lys 80
Arg	Asn	Gln	Lys	Thr 85	Thr	Val	Asn	Phe	Leu 90	Ile	Gly	Asn	Leu	Ala 95	Phe
Ser	Asp	Ile	Leu 100	Val	Val	Leu	Phe	Cys 105	Ser	Pro	Phe	Thr	Leu 110	Thr	Ser
Val	Leu	Leu 115	Asp	Gln	Trp	Met	Phe 120	Gly	Lys	Ala	Met	Cys 125	His	Ile	Met
Pro	Phe 130	Leu	Gln	Cys	Val	Ser 135	Val	Leu	Val	Ser	Thr 140	Leu	Ile	Leu	Ile
Ser 145	Ile	Ala	Ile	Val	Arg 150	Tyr	His	Met	Ile	Lys 155	His	Pro	Ile	Ser	Asn 160
Asn	Leu	Thr	Ala	Asn 165	His	Gly	Tyr	Phe	Leu 170	Ile	Ala	Thr	Val	Trp 175	Thr
Leu	Gly	Phe	Ala 180	Ile	Cys	Ser	Pro	Leu 185	Pro	Val	Phe	His	Ser 190	Leu	Val
Glu	Leu	Lys 195	Glu	Thr	Phe	Gly	Ser 200	Ala	Leu	Leu	Ser	Ser 205	Lys	Tyr	Leu
Cys	Val 210	Glu	Ser	Trp	Pro	Ser 215	Asp	Ser	Tyr	Arg	Ile 220	Ala	Phe	Thr	Ile
Ser 225	Leu	Leu	Leu	Val	Gln 230	Tyr	Ile	Leu	Pro	Leu 235	Val	Cys	Leu	Thr	Val 240
Ser	His	Thr	Ser	Val 245	Cys	Ile	Arg	Leu	Lys 250	Arg	Arg	Asn	Asn	Met 255	Met
Asp	Lys	Ile	Arg 260	Asp	Ser	Lys	Tyr	Arg 265	Ser	Ser	Arg	Ser	Arg 270	Ser	Val
Phe	Tyr	Arg 275	Leu	Thr	Ile	Leu	Ile 280	Leu	Val	Phe	Ala	Val 285	Ser	Trp	Met
Pro	Leu 290	His	Val	Phe	His	Val 295	Val	Thr	Asp	Phe	Asn 300	Asp	Asn	Leu	Ile
Ser 305	Asn	Arg	His	Phe	Lys 310	Leu	Val	Tyr	Cys	Ile 315	Cys	His	Leu	Leu	Gly 320
Met	Met	Ser	Cys	Cys 325	Leu	Asn	Pro	Ile	Leu 330	Tyr	Gly	Phe	Leu	Asn 335	Asn
Gly	Ile	Lys	Ala	Asp	Leu	Arg	Ala	Leu	Ile	His	Cys	Leu	His	Met	Ser

<210> 24

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Y1/Y5 CHIMERA

<400> 24

Met Asp Val Leu Phe Phe His Gln Asp Ser Ser Met Glu Phe Lys Leu
1 5 10 15

Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu Asn Asn Thr Ala Ala 20 25 30

Ala Arg Asn Ala Ala Phe Pro Ala Trp Glu Asp Tyr Arg Gly Ser Val 35 40 45

Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu 50 55 60

Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Val Met Lys Lys 65 70 75 80

Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe \$85\$ 90 95

Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser

Val Leu Leu Asp Gln Trp Met Phe Gly Lys Ala Met Cys His Ile Met 115 120 125

Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile 130 135 140

Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn 145 150 155 160

Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr \$165\$ \$170\$ \$175\$

Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val
180 185 190

Glu Leu Lys Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Lys Tyr Leu 195 200 205

Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile 210 215 220

Ser Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val 230 Ser His Thr Ser Val Cys Arg Ser Ile Ser Cys Gly Leu Ser His Lys Glu Asn Arg Leu Glu Glu Asn Glu Met Ile Asn Leu Thr Leu Gln Pro Ser Lys Lys Ser Arg Asn Gln Ala Lys Thr Pro Ser Thr Gln Lys Trp Ser Tyr Ser Phe Ile Arg Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala Pro Ala Gly Pro Ser Gln Gly Lys His Leu Ala Val Pro Glu Asn Pro Ala Ser Val Arq Ser Gln Leu Ser Pro Ser 330 Ser Lys Val Ile Pro Gly Val Pro Ile Cys Phe Glu Val Lys Pro Glu Glu Ser Ser Asp Ala His Glu Met Arg Val Lys Arg Ser Ile Thr Arg Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro Leu His Val Phe His Val Val 395 Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Lys Gln Arg Asp Leu Gln Phe Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp Tyr Glu 455 Thr Ile Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu 465 470 475

Lys Gln Ala Ser Pro Val Ala Phe Lys Lys Ile Ser Met Asn Asp Asn

490

495

Glu Lys Ile

485

<210> 25 <211> 395

- <212> PRT
- <213> Artificial Sequence
- <220>
- <223> Description of Artificial Sequence: Y1/Y5 CHIMERA
- <400> 25
- Met Asp Val Leu Phe Phe His Gln Asp Ser Ser Met Glu Phe Lys Leu 1 5 10 15
- Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu Asn Asn Thr Ala Ala 20 25 30
- Ala Arg Asn Ala Ala Phe Pro Ala Trp Glu Asp Tyr Arg Gly Ser Val\$35\$ 40 45
- Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu 50 60
- Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Val Met Lys Lys 65 70 75 80
- Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe 85 90 95
- Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser 100 105 110
- Val Leu Leu Asp Gln Trp Met Phe Gly Lys Ala Met Cys His Ile Met 115 120 125
- Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile 130 $$135\$
- Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn 145 150 155 160
- Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr 165 170 175
- Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val 180 185 190
- Glu Leu Lys Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Lys Tyr Leu 195 200 205
- Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile 210 215 220
- Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val 225 230 235 240
- Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg Arg Asn Asn Met Met
 245 250 255
- Asp Lys Ile Arg Asp Ser Lys Tyr Arg Ser Ser Arg Ser Arg Ser Val $260 \hspace{1cm} 265 \hspace{1cm} 270 \hspace{1cm}$

Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met 275 280 285

Pro Leu His Val Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile 290 295 300

Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly 305 310 315 320

Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn 325 330 335

Gly Ile Lys Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe Cys Asp Phe 340 345 350

Arg Ser Arg Asp Asp Tyr Glu Thr Ile Ala Met Ser Thr Met His 355 360 365

Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala Phe 370 375 380

Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Ile 385 390 395

<210> 26

<211> 341

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 26

Met Gly Ser Glu Ile Pro Asp Tyr Tyr Asn Lys Thr Leu Ala Ser Glu $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Asn Asn Thr Val Ala Thr Arg Asn Ser Gly Phe Pro Val Trp Glu Asp 20 25 30

Tyr Lys Gly Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr 35 40 45

Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met 50 55 60

Ala Val Met Arg Lys Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile
65 70 75 80

Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro 85 90 95

Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val

Met Cys His Ile Met Pro Phe Leu Gln Cys Val Thr Val Leu Val Ser

115 120 125

Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys 130 135 140

His Pro Val Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile 145 150 155 160

Ala Thr Val Trp Thr Leu Gly Leu Ala Ile Cys Ser Pro Leu Pro Val 165 170 175

Phe His Ser Leu Val Glu Leu Gln Glu Ser Phe Gly Ser Ala Trp Leu 180 185 190

Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg 195 200 205

Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu 210 215 220

Val Cys Leu Thr Val Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg 225 230 235 240

Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser 245 250 255

Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Val Leu Ile Leu Val Phe 260 265 270

Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val Thr Asp Phe 275 280 285

Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile 290 295 300

Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr 305 310 315 320

Gly Phe Leu Asn Asn Gly Ile Lys Ala Asp Leu Met Ser Leu Ile His 325 330 335

Cys Leu His Val Ser 340

<210> 27

<211> 383

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Y1/Y5 CHIMERA

<400> 27

Met Gly Ser Glu Ile Pro Asp Tyr Tyr Asn Lys Thr Leu Ala Ser Glu
1 5 10 15

Asn Asn Thr Val Ala Thr Arg Asn Ser Gly Phe Pro Val Trp Glu Asp 20 25 30

Tyr Lys Gly Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr 35 40 45

Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met 50 55 60

Ala Val Met Arg Lys Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile
65 70 75 80

Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro 85 90 95

Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val 100 105 110

Met Cys His Ile Met Pro Phe Leu Gln Cys Val Thr Val Leu Val Ser 115 120 125

Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys 130 135 140

His Pro Val Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile 145 150 155 160

Ala Thr Val Trp Thr Leu Gly Leu Ala Ile Cys Ser Pro Leu Pro Val 165 170 175

Phe His Ser Leu Val Glu Leu Gln Glu Ser Phe Gly Ser Ala Trp Leu 180 185 190

Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg 195 200 205

Ile Ala Phe Thr Ile Ser Leu Leu Val Gln Tyr Ile Leu Pro Leu 210 215 220

Val Cys Leu Thr Val Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg 225 230 235 240

Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Val Leu Ile Leu Val Phe 260 265 270

Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val Thr Asp Phe 275 280 285

Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile 290 295 300

Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr 305 310 315 320

Gly Phe Leu Asn Asn Gly Ile Gln Arg Asp Leu Gln Phe Phe Phe Asn 330 Phe Cys Asp Phe Arg Ser Arg Asp Asp Tyr Glu Val Ile Ala Met 345 Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala Leu Lys Lys Ile His Ser Asp Asp Asn Glu Lys Ile 375 <210> 28 <211> 21 <212> DNA <213> Homo sapiens <400> 28 21 ttttggttgc tgacaaatgt c <210> 29 <211> 26 <212> DNA <213> Homo sapiens <400> 29 26 ccttggtaaa cagtgagaat tattac <210> 30 <211> 455 <212> PRT <213> Cercopithecus aethiops <400> 30 Met Ser Phe Tyr Ser Lys Gln Asp Tyr Asn Met Asp Leu Glu Leu Asp 10 Glu Tyr Tyr Asn Lys Thr Leu Ala Thr Glu Asn Asn Thr Ala Ala Thr 25 Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp 40 Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu 55 Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg 75 70 Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val

105

Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu 165 170 175

Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu 180 185 190

Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys 195 200 205

Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser 210 215 220

Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser 225 230 230 235 240

His Thr Ser Val Cys Arg Ser Ile Ser Cys Gly Leu Ser Asn Lys Glu 245 250 255

Asn Arg Leu Glu Glu Asn Glu Met Ile Asn Leu Thr Leu His Pro Ser 260 265 270

Arg Lys Ile Gly Pro Gln Val Lys Leu Ser Gly Ser His Lys Trp Ser 275 280 285

Tyr Ser Phe Ile Lys Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala 290 295 300

Cys Val Leu Pro Ala Pro Glu Arg Pro Ser Gln Glu Asn His Ser Arg 305 310 315 320

Ile Leu Pro Glu Asn Phe Gly Ser Val Arg Ser Gln Leu Ser Ser Ser 325 330 335

Ser Lys Phe Ile Pro Gly Val Pro Thr Cys Phe Glu Ile Lys Pro Glu 340 345 350

Glu Asn Ser Asp Val His Glu Leu Arg Val Lys Arg Ser Val Thr Arg

Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile 370 375 380

Leu Val Phe Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val 385 390 395 400

Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val 405 410 415

gtaataattc tcactgttta ccaagg

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Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro
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 Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Lys Ala Asp Leu Met Ser
                             440
 Leu Ile His Cys Leu His Met
     450
                         455
 <210> 31
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 <212> DNA
 <213> Cercopithecus aethiops
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tgatttccca gtctgggatg actataaaag cagtgtagat gacttacagt attttctgat 180
tgggctctat acatttgtaa gtcttcttgg ctttatgggg aatttactta ttttaatggc 240
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ttcatacaga attgccttta ctatctcttt attgctagtt cagtatattc tgcccttagt 720
ttgtcttact gtaagtcata caagtgtctg cagaagcata agctgtggat tgtccaacaa 780
agaaaacaga cttgaagaaa acgagatgat caacttaact cttcatccat ctagaaagat 840
tgggcctcag gtgaaactct ctggcagcca taaatggagt tattcattca tcaaaaaaca 900
cagaaggaga tatagcaaga agacagcatg tgtgttacct gctccagaaa gaccttctca 960
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agatgttcat gaattgagag taaaacgttc tgttacaaga ataaaaaaga gatctcgaag 1140
tgttttctac aggctgacca tactgatact agtatttgct gttagttgga tgccactaca 1200
ccttttccat gtggtaactg attttaatga caatcttatt tcaaataggc atttcaagtt 1260
ggtgtattgc atttgtcatt tgttgggcat gatgtcctgt tgtcttaatc caattctgta 1320
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